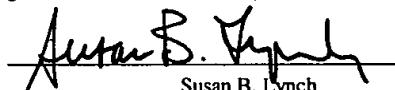


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PATENT
Docket No. 511582001601

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Susan B. Lynch

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Daniel E. AFAR et al.

Serial No.: 10/010,667

Filing Date: 06 December 2001

For: PEPTIDES DERIVED FROM STEAP1
(AS AMENDED)

Examiner: To be assigned

Group Art Unit: To be assigned

RESPONSE TO NOTICE TO FILE CORRECTED APPLICATION PAPERS

Box Sequence
Assistant Commissioner for Patents
P.O. Box 2327
Arlington, VA 22202

Dear Sir:

This is in response to the Notice to file Corrected Application Papers of nonprovisional application 10/010,667 mailed January 29, 2002, for which a response is due on March 29, 2002. Accordingly, this response is timely filed.

Please enter the following Sequence Listing, amendments and remarks.

In the Sequence Listing:

Please insert the attached paper copy of the Sequence Listing as new pages 1-10 in the above-captioned application. A computer-readable form copy (CRF copy) of the Sequence Listing accompanies this response.

AMENDMENTSIn the Specification

Please replace the paragraph beginning at page 5, line 35, with the following rewritten paragraph:

C1
 FIG. 4-1- 4-2. Nucleotide sequence of STEAP-1 GTH9 clone (SEQ ID NO:6) corresponding to the 4 kb message on northern blots (FIG. 3A). The sequence contains an intron of 2399 base pairs relative to the STEAP-1 clone 10 sequence of FIG. 1A; coding regions are nucleotides 96-857 and 3257-3510 (indicated in bold). The start ATG is in bold and underlined, the STOP codon is in bold and underlined, and the intron-exon boundaries are underlined.--

C2
 Please replace the paragraph beginning at page 7, line 23, with the following rewritten paragraph:

-- FIG. 11. Primary structural comparison of STEAP family proteins. FIG. 11A. Amino acid sequence alignment of STEAP-1 (8P1D4 CLONE 10; SEQ ID NO:2) and STEAP-2 (98P4B6;SEQ ID NO: 8) sequences. The alignment was performed using the SIM alignment program of the Baylor College of Medicine Search Launcher Web site. Results show a 61.4% identity in a 171 amino acid overlap; Score: 576.0; Gap frequency: 0.0%. FIG. 11B. Amino acid sequence alignment of STEAP-1 with partial ORF sequences of STEAP-2 and two other putative family member proteins using PIMA program (PIMA 1.4 program at Internet address <<http://dot.imgen.bcm.tmc.edu:9331/multi-align/multi-align.html>>); transmembrane domains identified by the SOSUI program (available at Internet address <http://www.tuat.ac.jp/~mitaku/adv_sosui/submit.html>). are in bold.--